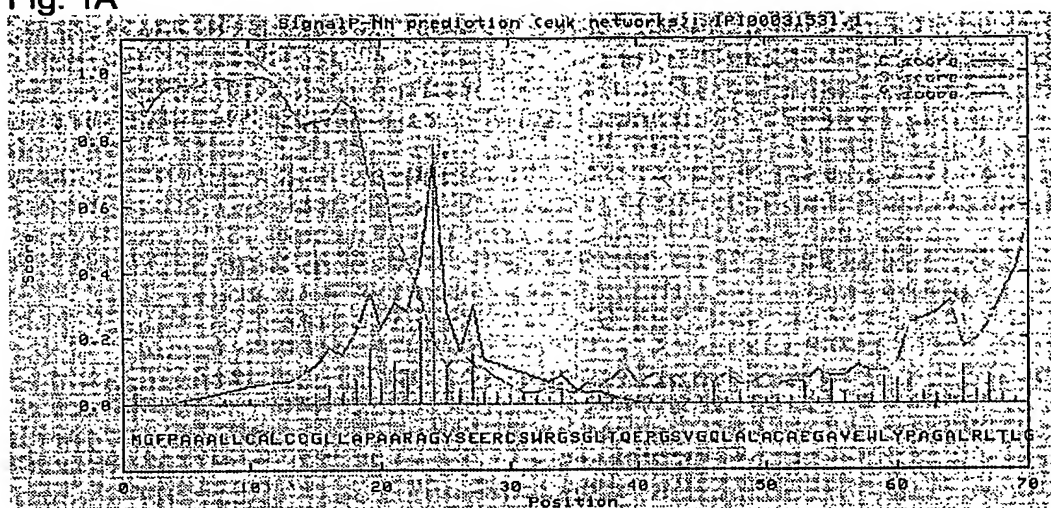


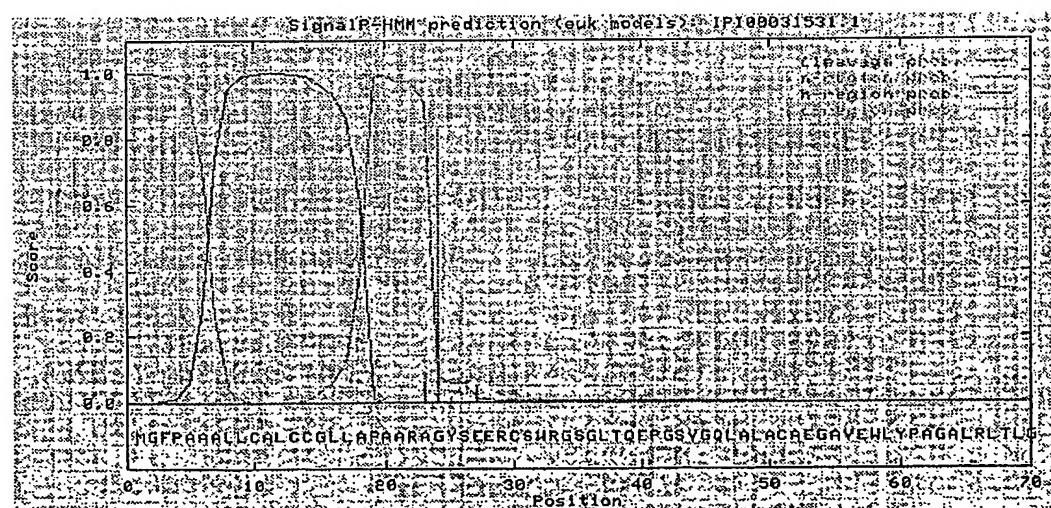
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Fig. 1A



```
>IPI00031531.1          length = 293
# Measure  Position  Value  Cutoff  signal peptide?
max. C      24       0.785  0.33   YES
max. Y      24       0.746  0.32   YES
max. S      11       0.989  0.82   YES
mean S      1-23     0.846  0.47   YES
# Most likely cleavage site between pos. 23 and 24: ARA-GY
```

Fig. 1B



```
>IPI00031531.1
Prediction: Signal peptide
Signal peptide probability: 1.000
Signal anchor probability: 0.000
Max cleavage site probability: 0.832 between pos. 23 and 24
```

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**FIG. 2****human Nsg33 (SEQ ID No 3)**

# Gene Ontology category	Odds
Signal_transducer	0.538
Receptor	0.433
Hormone	<b>1.173</b>
Structural_protein	0.168
Transporter	0.230
Ion_channel	0.372
Voltage-gated_ion_channel	0.130
Cation_channel	0.215
Transcription	0.294
Transcription_regulation	0.152
Stress_response	0.340
Immune_response	0.186
Growth_factor	<b>2.083</b>
Metal_ion_transport	0.020

**human N-terminal peptide (SEQ ID No 19)**

# Gene Ontology category	Odds
Signal_transducer	0.464
Receptor	0.296
Hormone	0.206
Structural_protein	0.987
Transporter	0.311
Ion_channel	0.147
Voltage-gated_ion_channel	0.157
Cation_channel	0.215
Transcription	0.311
Transcription_regulation	0.829
Stress_response	0.162
Immune_response	1.460
Growth_factor	<b>8.142</b>
Metal_ion_transport	0.061

**human C-terminal peptide (SEQ ID No 5)**

# Gene Ontology category	Odds
Signal_transducer	0.242
Receptor	0.038
Hormone	0.303
Structural_protein	0.096
Transporter	0.231
Ion_channel	0.185
Voltage-gated_ion_channel	0.191
Cation_channel	0.215
Transcription	0.312
Transcription_regulation	0.295
Stress_response	0.145
Immune_response	0.157
Growth_factor	<b>7.963</b>
Metal_ion_transport	0.020

**Fig 3a. CLUSTAL W (1.82) multiple sequence alignment**

Mouse NsG33 **HASAHASALLCALCCGLLAASAHAGYSEDRCSWRGSGLTQEPGSVGQLTLDCTEGAIEWL**  
Rat NsG33 **---MLVAALLCALCCGLLAASARAGYSEDRCSWRGSGLTQEPGSVGQLTLDCTEGAIEWL**  
Human NsG33 **-MGFPAAALLCALCCGLLAPARAGYSEERCSWRGSGLTQEPGSVGQLALACAEGAVEWL**  
**.:\*\*\*\*\*.:\*:\*\*\*\*:\*\*\*\*\*:\*\*\*\*\*.:\* \*:\*\*\*:\*\*\***

Mouse NsG33 **YPAGALRLTLGGPDGPTRPSIVCLRPERPFAGAQVFAERMTGNLELLLAEGPDLAGGRCM**  
Rat NsG33 **YPAGALRLTLGGSDGPTRPSIVCLRPTRFAGAQVFAERMAGNLELLLAEGQGGLAGGRCM**  
Human NsG33 **YPAGALRLTLGGPDPRARPGIACLRPVRPFAGAQVFAERAGGALELLLAEGGPGPAGRCV**  
**\*\*\*\*\*:\*\*\*:\*\*\*:\*\*\*\*\* \*\*\*\*\* \***

Mouse NsG33 **RWGPRRERALFLQATPHRDISRRVAAFRELHEDQRAEMSPQAQGLVDGACRPCSDAEL**  
Rat NsG33 **RWGPRRERALFLQATPHRDISRRVAAFRELHEDQRAEMSPQAQGFVDGACRPCSDAEL**  
Human NsG33 **RWGPRRERALFLQATPHQDISRRVAAFRELREDGRPELPPQAHGLVDGACRPCSDAEL**  
**\*\*\*\*\*:\*\*\*\*\*:\*\*\*:\*\*\* \*:\*.\*\*\*:\*.\*\*\*\*\***

Mouse NsG33 **LLAACTSDFVIHGTHIGVAHDTELQESVITVVVARVIRQTLPLFKEGSSEGGQGRASIRTL**  
Rat NsG33 **LLTACTSDFVIHGTHIGVVHDMELQESVITVVATRIVIRQTLPLFQEGSSEGRGQASVRTL**  
Human NsG33 **LLAACTSDFVIHGIHGVTHDVELQESVITVVAARVIRQTPPLFQAGRSGDQGLTSIRTP**  
**\*\*.\*\*\*\*\*\* \*\*\*\*\*.\* \*\*\*\*\*:\*\*\*:\*\*\* \*\*:\*.\*\*\*:\*\*\***

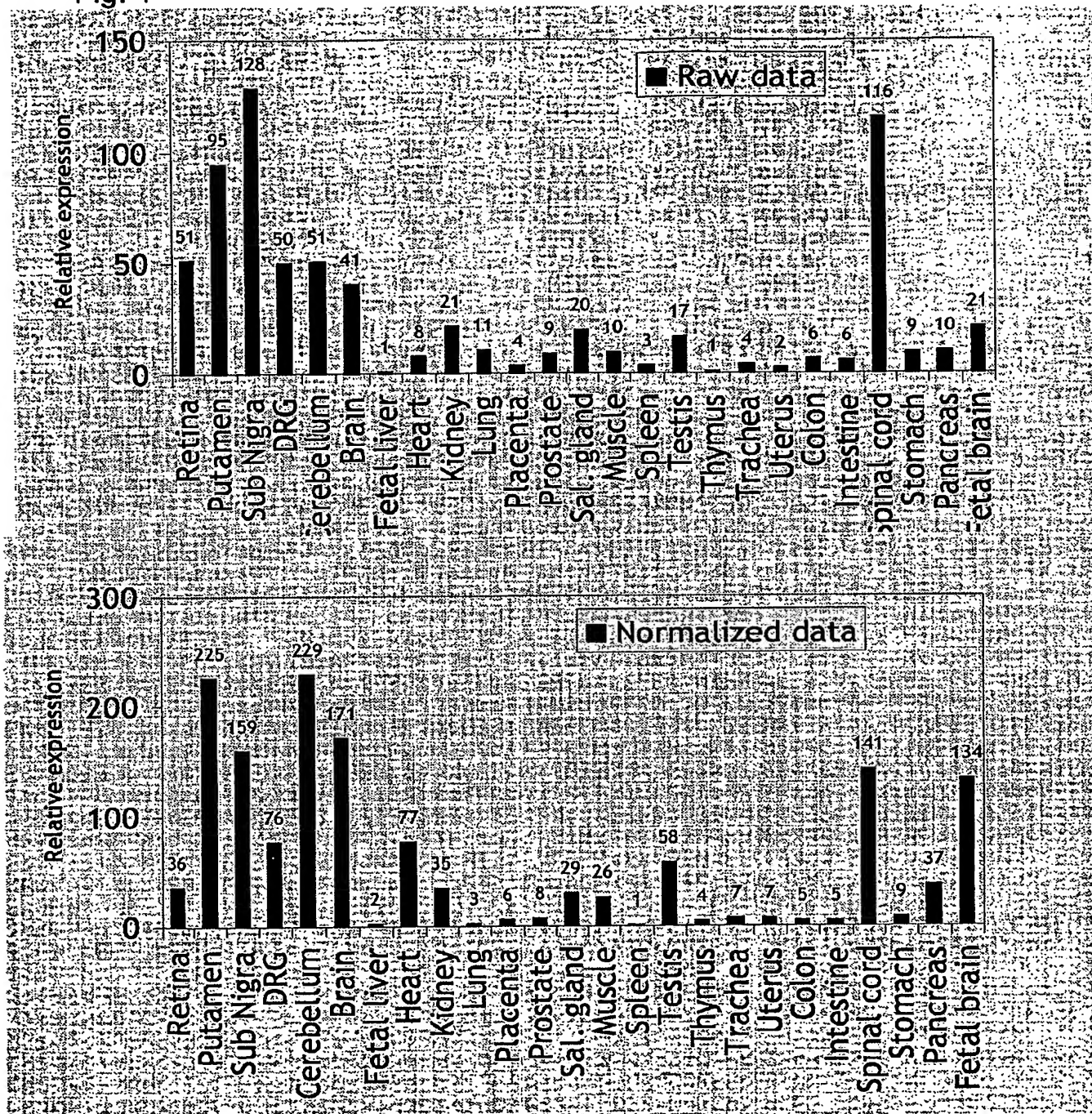
Mouse NsG33 **LCRCVVRPGPGSFLFMGWSRFGEAWLGCAPRFQEFESRVYSAAALTHLNPCEMALD**  
Rat NsG33 **LCRCVVRPGPGSFLFMGWSRFGEAWLGCAPRFQEFESRVYSAAALAHLNPCEVALD**  
Human NsG33 **LCRCVHPGPGTFLFMGWSRFGEARLGCAPRFQEFRRAYEAARAAHLHPCEVALH**  
**\*\*\*\*\*:\*\*\*\*\* \*\*\*\*\* \*.\*.\*\*\*:\*\*\*:\*\*\***

**Fig 3b. CLUSTAL W (1.82) multiple sequence alignment**

Mouse	--MLVATLLCALCCGLLAASAHAGYSEDRCSWRGSGLTQEPGSGVQGLTLDCTEGAIEWLY	58
Rat	--MLVAALLCALCCGLLAASARAGYSEDRCSWRGSGLTQEPGSGVQGLTLDCTEGAIEWLY	58
Human	MGFPAALLCALCCGLLAPAAAGYSEERCSWRGSGLTQEPGSGVQLALACAEGAVEWLY	60
	: .*:*****.*:*****:*****.* *:***:****	
Mouse	PAGALRLTLGGPDPGTRPSIVCLRPERPFAGAQVFAERMTGNLELLLAEGPDLAGGRCMR	118
Rat	PAGALRLTLGGSDPGTRPSIVCLRPRPFAGAQVFAERMAGNLELLLAEGQGLAGGRCMR	118
Human	PAGALRLTLGGPDPRARPGIACLRPVPFAGAQVFAERAGGALLAEGFGPGAGGRCVR	120
	*****.*.* .*:**** ***** * ***** . *****:*	
Mouse	WGPRERRALFQATPHRDISRRVAAFRFELHEDQRAEMSPQAQGLVDGACRPCSDAELL	178
Rat	WGPRERRALFQATPHRDISRRVAAFQFELHEDQRAEMSPQAQGFVDGACRPCSDAELL	178
Human	WGPRERRALFQATPHQDISRRVAAFRFELREDGRPELPPQAHGLVDGACRPCSDAELL	180
	*****.*:*****:***:* .*: .***:*:*****	
Mouse	LAACTSDFVIHGTHINGVAHDTLQESVITVVVARVIRQTLPLFKEGSSEGGQGRASIRTL	238
Rat	LTACTSDFVIHGTHINGVVDHDELQESVITVVATRIVIRQTLPLFQEGSSEGRGQASVRTL	238
Human	LAACTSDFVIHGIHGVTHDVELQESVITVVAARVLRTPLPFQAGRSGDQGLTISIRTP	240
	*:***** ****.* *****.:**:* ***: * * .*: :*:*	
Mouse	RCGVPRPGGSFLFMGWSRFGEAWLGCAPRFQEFSSRVYSAALTHLNPCEMALD	291
Rat	RCGVPRPGGSFLFMGWSRFGEAWLGCAPRFQEFSSRVYSAALAAHLNPCEVALD	291
Human	RCGVHPGPGTFLFMGWSRFGEARLGCAPRFQEFRRAYEAARAAHLHPCEVALH	293
	***-***:***** ***** * * * :*:*****:***	

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Fig. 4



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scoring matrix: BLOSUM50, gap penalties: -12/-2  
 42.3% identity; Global alignment score: 747

```

      10      20      30      40      50 *
Innog. MRGAARAAWGRAGQPWPRPPAPGPPPPPLPLLLLLLAGLLGGAG-AQYSSDRCSWKGSGL
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  -----MGFPAAALLCALCCGLLAPAAARAGYSEERCSSWRGSGL
                        10      20      30

      60      70      *  80      90      100      *110
Innog. THEAHRKEVEQVYLRCAAGAVEWMYPTGALIVNLR-PNTFSPARHLTVCI RSFTDSSGAN
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  TQEPGS--VGQIALACAEGAVEWLYPAGALRLTLGGPDPR--ARPGIACLRPVRPFAGAQ
      40      50      60      70      80      90

      120     130     140 *  150     160     170
Innog. IYLEKTG-ELRLLPDGDGRPGRVQC--FG-LEQGGLFVEATPQQDIGRRTTG FQYELVR
      .. :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  VFAERAGGALELLLAEGPG-PAGGRCVRWGPRERRALFLQATPHQDISRRVA AFRFELRE
      100     110     120     130     140     150

      180     190     200     210     220
Innog. RHRAS---DLHEL SAP--CRPCSDTEVLLAVCTSDFAVRGSIQQVTHEPERQDS AIHLRV
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  DGRPELPFQA HGLGVDGACRPCSDAELLAACTSDFVIHGIIHGVTHDVELQESVITVVA
      160     170*  *  180  *  190     200     210

      230     240     250     260     270     280
Innog. SRLYRQKSRVFEPVPEGDGHWQG--RVRTLLECGVRPGHGDFLFTGHMHFG EARLGCAPR
      .. :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  ARVLRQT PPLFQAGRSGD--QGLTSIRTPLRCGVHPGPGTFLFMGWSRFGEARLGCAPR
      220     230     240 *  250     260     *

      290     300     *  310
Innog. FKDFQRM YRDAQERGLNPCEVGTD
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
NsG33  FQEFRRAYEA ARAAHLHPCEVALH
      270     280     290

```

Fig 5

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```

1  gcttcgccg ggcgcggcgg ccggcgcccc cggctgctcc cggcgccgcc cggaccgcgg ccgcgcgcgg gcagcgggtgg tgagagcccc gactcccccgg
101 acgcgcgcgc cagtgcacatg gggtttcccg ccgcggcgct gctctgcgcg cttgtctgcg gcctcctggc ccggtctggc ccgcccggct actccgagga
    >>.....CDS.....
201 gcgctgcagc tggaggggca gcgcctcac ccaggagccc ggcagcgtgg ggcagctggc cctggcctgt gcggaggggc cgtttgagtg gctgtacccg
    >.....CDS.....
    m g f p a a a l l c a l c c g l l a p a a r a g y s e
    >.....CDS.....
301 e r c s w r g s g l t q e p g s v g q l a l a c a e g a v e w l y p
    >.....CDS.....
    gctggggcgc tgcgcctgac cctggggcgc ccgcatccca gagcgcggcc cggcatgcgc tgtctgcgc cgttcgcggc cttgcgcggc gcccaggtct
    >.....CDS.....
    a g a l r l t l g p d p r a r p g i a c l r p v r p f a g a q v
401 tcgcggagcg cgcagggggc gccctggagc tgctgtggc caggggcgc ggcgcggcag ggggcgcgtg cgtgcgtgg ggtccccgcg agcgcgcggc
    >.....CDS.....
    f a e r a g g a l e l l l a e g p g p a g g r c v r w g p r e r
501 cctcttctcg caggccacgc cgcaccagga catcagccgc cgcgtggcgc cttccgctt tgagctgcgc gaggaacggc gcccgagct gcccccgcag
    >.....CDS.....
    a l f l q a t p h q d i s r r v a a f r f e l r e d g r p e l p p q
601 gcccaaggtc tggcgctaga cgtgcctgc aggcctgca ggcgcgtga gctgctctg gccgcctgca ccagcgactt cgtaattcac gggatcatcc
    >.....CDS.....
    a h g l g v d g a c r p c s d a e l l l a a c t s d f v l h g i l
701 atggggtcac ccatgacgtg gagctgcagg agtctgtcat cactgtggtg gccgcgcgtg tcctccgcca gacaccgcgc ctgttcagg cggggcgatc
    >.....CDS.....
    h g v t h d v e l q e s v i t v v a a r v l r q t p p l f q a g r
801 cggggaccag gggctgacct ccattcgtac ccactgcgc tgtggcgtcc acccgggccc aggcaccttc ctcttcattg gctggagccg ctttggggag
    >.....CDS.....
    s g d q g l t s i r t p l r c g v h p g p g t f l f m g w s r f g e
901 gcccggtgg gctgtgccc acgattccag gattccgcc gtgcctacga ggtgcccgt gctgcccacc tcaccccctg cgaggtggcg ctgcactgag
    >.....CDS.....
    a r l g c a p r f q e f r r a y e a a r a a h l h p c e v a l h -
1001 gggctgggtg ctggggaggg gctggtagga gggagggtgg gccactgct ttggaggtga tgggactatc aataagaact ctgttcacgc aaaaaaaaaa
1101 aaaaaaaaaa

```

Fig 6

1 ccaagcgtcc gccacgcgct ccgcgcttct ttgcgcgctc tgttgccgcc tcttgccgcg gtcgcgtcac gctgggtact cggaagaccg ctgcagctgg  
 >>.....CDS.....>  
 101 h a s a h a s a l l c a l c c g l l a a s a h a g y s e d r c s w  
 aggggcagcg gtttgaccga ggagcctggc agcgtggggc agctgaccct ggactgtact gagggcgcta togagtggct gtaccagct ggggcgctgc  
 >.....CDS.....>  
 201 r g s g l t q e p g s v g q l t l d c t e g a i e w l y p a g a l  
 gctgaccct gggggccccc gatccgggca cagggccacg catcgtctgt ctgcgcccag agcggccctt cgctggtgcc caggtctctcg ctgaacgtat  
 >.....CDS.....>  
 301 r l t l g g p d p g t r p s i v c l r p e r p f a g a q v f a e r  
 gacgggcaat ctagagtgc tactggccga gggccgggac ctggctgggg gcgctgcat gcgctggggt cccgcgcagc gcgcagccct ttctctgcag  
 >.....CDS.....>  
 401 m t g n l e l l l a e g p d l a g g r c m r w g p r e r a l f l q  
 gccacaccac accgcgcaat cagccgcaga gttgctgcct tccgttttga actgcacag gaccaacgtg cagaaatgc tcccaggt caaggtcttg  
 >.....CDS.....>  
 501 a t p h r d i s i r v a a f r f e l h e d q r a e m s p q a q g l  
 gtgtggatgg tgcctgcagg ccctgcagtg atgcgcagct cctcctggct cctgcacca gtgattttgt gatccacggg accatccatg gggtcgcccc  
 >.....CDS.....>  
 601 g v d g a c r p c s d a e l l l a a c t s d f v i h g t i h g v a  
 tgacacagag ctgcaagaat cagtcacac tgtgtgtgtt gctcgtgtca tccgcacag actgccactg ttcaagggaag ggagctcgga gggccaaagg  
 >.....CDS.....>  
 701 h d t e l q e s v i t v v v a r v i r q t l p l f k e g s s e g q g  
 cgggcctcca ttgtacett gctgcgctgt ggtgtgcgtc ctggccacgg ctccttcctc ttcatgggt ggagccgatt tggcgaagct tggctgggt  
 >.....CDS.....>  
 801 r a s i r t l l r c g v r p g p g s f l f m g w s r f g e a w l g  
 gtgctcccg cttccaagag ttacgcccgtg tctattcagc tgctctcacg acccatctca acccatgtga gatggcactg gactgagaga cctggggagca  
 >.....CDS.....>  
 901 c a p r f q e f s r v y s a a l t t h l n p c e m a l d -  
 agcctggat ggaccttctt ctggagatgg ggtgttggg aggtgtatgg gaggtgggt gagaaggggt tggctcggat ggcatcctgg taccacagt  
 1001 gagctggtag aatactaagt aatctggacc ataaaaaaa aaaaaaa

Fig 7a

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```

1  gggcagccgc gccgcgggct gctgcgcgtg cggccccgcac cctccccggg cagcagtcgc aggccccggc gcgtccccta accatgctgg
   >>CDS.>
   m 1
91  tagcaacgct tctttggcgc ctctgttgcg gcctctctggc cggctccgct cagctggct actcgaaga cgcctgcagc tggaggggca
   >.....CDS.....>
   v a t l i c a l c c g l l a s a h a g y s e d r c s w r g
181  gcggtttgac ccaggagcct ggcagcgtgg ggcagctgac cctggactgt actgaggcg ctatcgagt gctgtaccca gctggggcgc
   >.....CDS.....>
   s g l t q e p g s v g q l t l d c t e g a l e w l y p a g a
271  tgcgcctgac cctggggcgc ccgcatcgg gcacacggcc cagcatcgtc tgcctgcgc cagagggcc cttcgtggt gcccaggtct
   >.....CDS.....>
   l r l t l g g p d p g t r p s i v c l r p e r p f a g a q v
361  tcgtgaacg tatgacggc aatctagat tgctactggc cgaggcccg gacctggctg gggccgctg catgcgctg ggtccccgcg
   >.....CDS.....>
   f a e r m t g n l e l l l a e g p d l a g g r c m r w g p r
451  agcgcgagc ccttttctg caggccacac cacacgcga catcagcgc agagtgtgct ccttcogtt tgaactgcac gaggaccaac
   >.....CDS.....>
   e r x a l f l q a t p h r d l s r r v a a f r f e l h e d q
541  gtgcagaaat gtctcccag gtccaagtc ttggttgga ttggtcctgc aggccctgca gtgatgccga gctcctctg gctgcatgca
   >.....CDS.....>
   r a e m s p g a q g l g v d g a c r p c s d a e l l l a a c
631  ccagtgttt ttgtatccac gggaccatcc atggggtgc ccatgacaca gagctgcaag aatcagtcac cactgtggtg gttgctcgtg
   >.....CDS.....>
   t s d f v i h g t i h g v a h d t e l q e s v i t v v a r
721  tcatecgcca gacactgcca ctgttcaagg aaggagctc ggagggcaa ggcggggcct ccattgtac cttgctggc tgttgtgtgc
   >.....CDS.....>
   v i r q t l p l f k e g s s e g q g r a s i r t l l r c g v
811  gtctcggccc aggtccttc ctcttcattg gctggagccg atttgcgaa gctgggctgg gctgtgtcc ccgttccaa gattcagcc
   >.....CDS.....>
   x p g p g s f l f m g w s r f g e a w l g c a p r f q e f s
901  gtgtctattc agctgcttc acgaaccatc tcaaccatg tgagatgcca ctggactgag agacctgga gaaagccctg gatggacctt
   >.....CDS.....>
   r v y s a a l t t h l n p c s m a l d -
991  ctctcggaga tggggtgttg gggagggtga tgggagggtg ggtgagaagg gttgggctcg gatgcatcc tggtaaccac agtgagctgg
1081  tagaatacta agtaacttgg accataccag ccactgtagt ctgtgtcttc ttgtgcaggc agcataccca gctctgtgc tgcctcactt
1171  tgtctactct ccagtctgct gcccttctaa cccttcttag cctgtgacc agtgagctca tgttttctc gaattccagg gtgtgtctgg
1261  ggttcagagc aacctgccc tagtttgga gacttgagct aattgtttt tttttgttg tttttttgtt tgtttaaagg tggcctgggg
1351  gggcgggcaa aca

```

Fig 7b



1 atgtctggttag cggcgcttct ctgcgcgctg tgctggggcc tcttggtgc gtcgcctoga gctggtact ccgaggaccg ctgcagctgg aggggcagcg  
 >>.....CDS.....>  
 101 m l v a a l l c a l c c g l l a a s a r a g y s e d r c s w r g s  
 gtttgaccca ggaacctggc agctggggc agctgacct ggattgtact gaggtgcta tcgagtggt gstatcagct gggcgctgc gcctgactct  
 >>.....CDS.....>  
 201 g l t q e p g s v g q l t l d c t e g a i e w l y p a g a l r l t  
 aggegctct gatccgggca cggggccag catcgtctgt ctgcgcca caeggcctt cgctgtgcc caggtcttcg ctgaacggat ggcgggcaac  
 >>.....CDS.....>  
 301 l g g s d p g t r p s i v c l r p t r p f a g a q v f a e r m a g n  
 ctgagttgc tactggcga gggccaaggc ctggctggg ggcgtgcat gcgtgggt cctcggagc ggcgagcct tttctgcag gccacggcac  
 >>.....CDS.....>  
 401 l e l l l a e g q g l a g g r c m r w g p r e r a l f l q a t p  
 accgggacat cagccgcga gttgctgcct tccaattga actgcacgag gaccaacgtg cagaaatgtc tcccaggcc caaggttttg gtgtggatgg  
 >>.....CDS.....>  
 501 h r d i s r v a a f q f e l h e d q r a e m s p q a q g f g v d  
 tgcctgcagg cctgcagtg atgcgagct ccttctgact gcatgcacca gtgactttgt gatccatggg accatccatg ggtctgtcca tgacatggag  
 >>.....CDS.....>  
 601 g a c r p c s d a e l l l t a c t s d f v i h g t i h g v v h d m e  
 ctgcaagaat cagtcateac tgtgtgggccc actcgtgtca tccgccagc actgcactg ttccaggag gtagctcga gggcggggc caggcctccg  
 >>.....CDS.....>  
 701 l q e s v l t v v a t r v i r q t l p l f q e g s s e g r g q a s  
 ttcgtacctt gttgcgtgt ggtgtgcgtc ctggcccagg ctcttctc ttcattggct ggagcagatt tggcgaagct tggctgggct gcgctcccg  
 >>.....CDS.....>  
 801 v r t l l r c g v r p g p g s f l f m g w s r f g e a w l g c a p  
 ctccaagag ttacgacgtg tctattcagc tgctctcgc gccacctca accaatgtga ggtggcactg gactgagaga cctggggagca agccctggat  
 >>.....CDS.....>  
 901 r f q e f s r v y s a a l a a h l n p c e v a l d -  
 ggatcttct ctgggggatgg ggtgttgggg aggggtgata ggggggtggg tgggaagggt gtggctcaga tggcatcctg gtaccacag tgaggtggta  
 1001 gaatactaaa taacctggat cacacc

Fig 8

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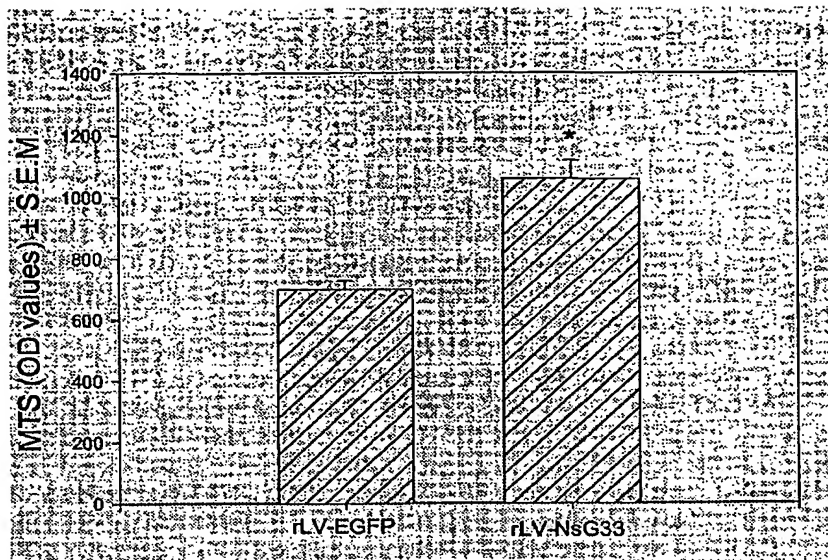


Fig. 9

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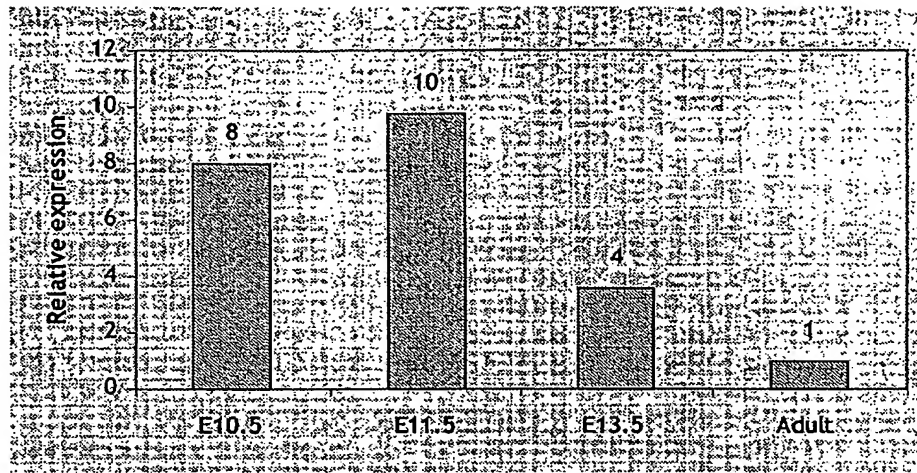


Fig. 10A

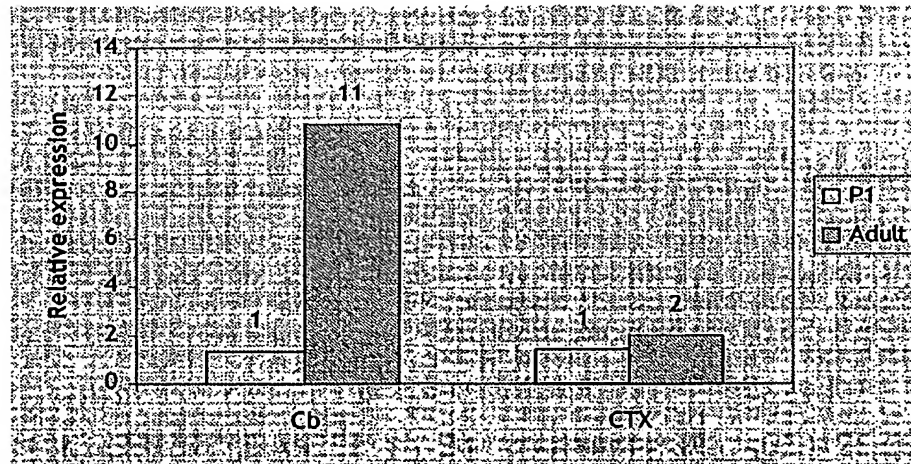


Fig. 10B

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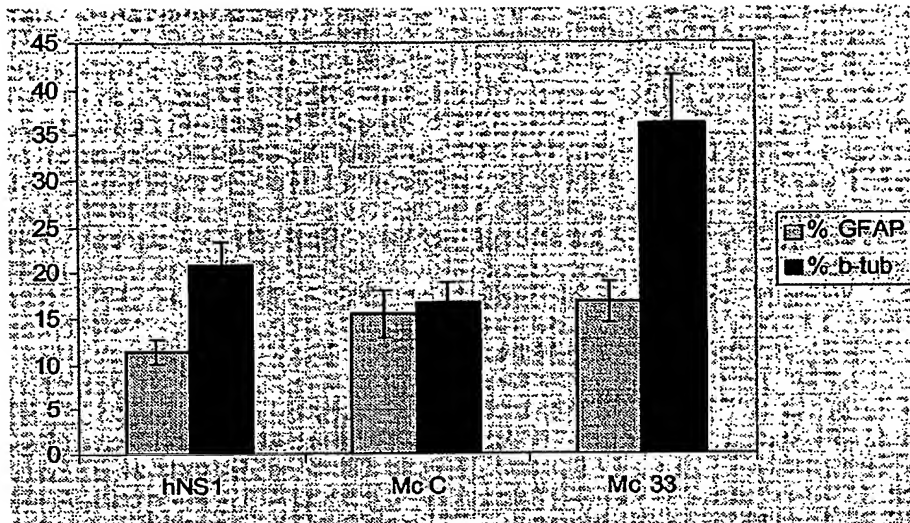


Fig. 11A

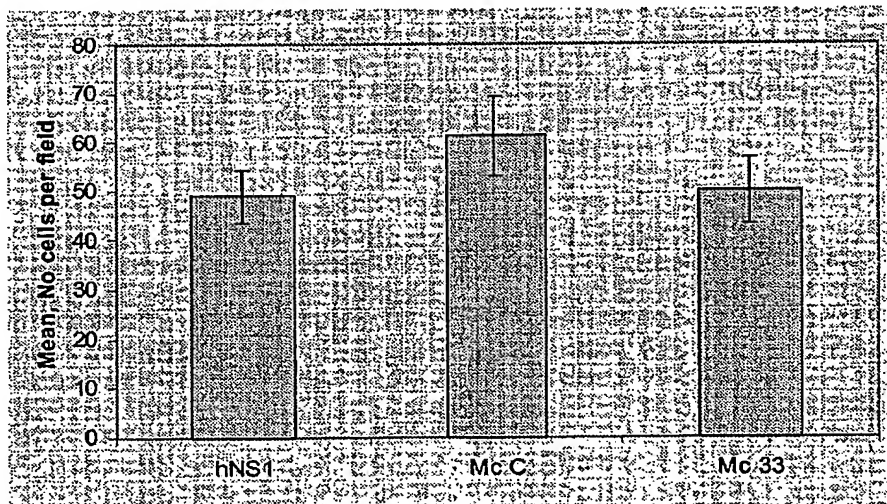


Fig. 11B

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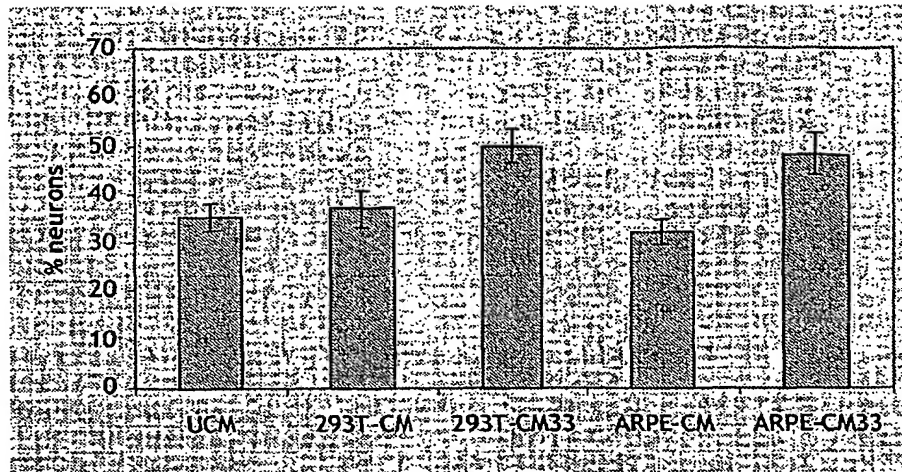


Fig. 12

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